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(FILE 'HOME' ENTERED AT 16:42:35 ON 21 JAN 96)

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 16:43:31 ON 21 JAN 96

L1 272 FILE MEDLINE

L2 256 FILE BIOSIS

L3 56 FILE CAPLUS

TOTAL FOR ALL FILES

L4 584 S BRENNER S/AU

L5 48 FILE MEDLINE

L6 42 FILE BIOSIS

L7 8 FILE CAPLUS

TOTAL FOR ALL FILES

L8 98 S L4 AND SEQUENC?

L9 56 DUP REM L8 (42 DUPLICATES REMOVED)

L10 0 FILE MEDLINE

L11 0 FILE BIOSIS

L12 0 FILE CAPLUS

TOTAL FOR ALL FILES

L13 0 S L4 AND SORT###

L14 22 FILE MEDLINE

L15 23 FILE BIOSIS

L16 27 FILE CAPLUS

TOTAL FOR ALL FILES

L17 72 S OLIGONUCLEOTIDE# (3A) TAG####

L18 36 DUP REM L17 (36 DUPLICATES REMOVED)

L19 197 FILE MEDLINE

L20 249 FILE BIOSIS

L21 167 FILE CAPLUS

TOTAL FOR ALL FILES

L22 613 S SORT### (3A) (CDNA OR DNA OR MRNA OR POLYNUCLEOTIDE# OR

L23 326 DUP REM L22 (287 DUPLICATES REMOVED)

=> s (multiplex or parallel) (3a) sequenc?

L24 129 FILE MEDLINE

L25 175 FILE BIOSIS

L26 297 FILE CAPLUS

TOTAL FOR ALL FILES

L27 601 (MULTIPLEX OR PARALLEL) (3A) SEQUENC?

=> s 127 and (nucleic or DNA or RNA or polynucleot?)

=> s l27 and nucleic

L28 38 FILE MEDLINE

L29 3 FILE BIOSIS

L30 23 FILE CAPLUS

TOTAL FOR ALL FILES

L31 64 L27 AND NUCLEIC

=> dup rem l31

PROCESSING COMPLETED FOR L31

L32 59 DUP REM L31 (5 DUPLICATES REMOVED)

L18 ANSWER 15 OF 36 MEDLINE

DUPLICATE 6

AU Needels M C; Jones D G; Tate E H; Heinkel G L; Kochersperger L M;  
Dower W J; Barrett R W; Gallop M A

TI Generation and screening of an oligonucleotide-encoded synthetic  
peptide library.

SO Proc Natl Acad Sci U S A, (1993 Nov 15) 90 (22) 10700-4.  
Journal code: PV3. ISSN: 0027-8424.

AB We have prepared a library of approximately 10(6) different peptide  
sequences on small, spherical (10-microns diameter) beads by the  
combinatorial chemical coupling of both L- and D-amino acid building  
blocks. To each bead is covalently attached many copies of a single  
peptide sequence and, additionally, copies of a unique  
single-stranded oligonucleotide that codes for that peptide  
sequence. The \*\*\*oligonucleotide\*\*\* \*\*\*tags\*\*\* are  
synthesized through a parallel combinatorial procedure that  
effectively records the process by which the encoded peptide  
sequence is assembled. The collection of beads was screened for  
binding to a fluorescently labeled anti-peptide antibody using a  
fluorescence-activated cell sorting instrument. Those beads to which  
the antibody bound tightly were isolated by fluorescence-activated  
sorting, and the oligonucleotide identifiers attached to individual  
sorted beads were amplified by the PCR. Sequences of the amplified  
DNAs were determined to reveal the identity of peptide sequences  
that bound to the antibody with high affinity. By combining the  
capacity for information storage in an oligonucleotide code with the  
tremendous level of amplification possible through the PCR, we have  
devised a means for specifying the identity of each member of a vast  
library of molecules synthesized from both natural and unnatural  
chemical building blocks. In addition, we have shown that the use of  
flow cytometry instrumentation permits facile isolation of  
individual beads that bear high-affinity ligands for biological  
receptors.

L23 ANSWER 57 OF 326 CAPLUS COPYRIGHT 1996 ACS  
IN Chetverin, Alexander B.; Kramer, Fred Russell  
TI Oligonucleotide arrays and their use for sorting, isolating,  
sequencing, and manipulating nucleic acids  
SO PCT Int. Appl., 103 pp.  
CODEN: PIXXD2  
AB Binary oligonucleotides having a const. nucleotide sequence adjacent  
to a variable nucleotide sequence are used for \*\*\*sorting\*\*\* and  
surveying \*\*\*nucleic\*\*\* acid strands. These oligonucleotide  
arrays are used for \*\*\*sorting\*\*\* mixt. of \*\*\*nucleic\*\*\*  
acid strands, making immobilized partial copies of nucleic acid  
strands, ligating strands, or introducing site directed mutations  
into strands. Information is obtained for detg. the sequence of a  
nucleic acid strand, alone or in a mixt., by generating partials of  
the strand and, for groups of partials having the same terminal  
variable oligonucleotide, sep. detg. the presence and sequence of  
all variable oligonucleotide. Arrays are also used to order  
previously sequenced nucleic acid fragments and to allocate ordered  
allelic fragments to chromosomal linkage groups.

=> d 57

L23 ANSWER 57 OF 326 CAPLUS COPYRIGHT 1996 ACS  
AN 1993:597263 CAPLUS  
DN 119:197263  
TI Oligonucleotide arrays and their use for sorting, isolating,  
sequencing, and manipulating nucleic acids  
IN Chetverin, Alexander B.; Kramer, Fred Russell  
PA Public Health Research Institute of the City of New York, Inc., USA  
SO PCT Int. Appl., 103 pp.  
CODEN: PIXXD2  
PI WO 9317126 A1 930902  
DS W: AT, AU, BB, BG, BR, CA, CH, DE, DK, ES, FI, GB, HU, JP, KP, KR,  
LK, LU, MG, MN, MW, NL, NO, PL, RO, RU, SD, SE  
RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, ES, FR, GA, GB, GR,  
IE, IT, LU, MC, ML, MR, NL, PT, SE, SN, TD, TG  
AI WO 93-US1552 930219  
PRAI US 92-838607 920219  
DT Patent  
LA English

L32 ANSWER 15 OF 59 CAPLUS COPYRIGHT 1996 ACS  
AU Egholm, Michael; Behrens, Carsten; Christensen, Leif; Berg, Rolf H.;  
Nielsen, Peter E.; Buchardt, Ole  
TI Peptide \*\*\*nucleic\*\*\* acids containing adenine or guanine  
recognize thymine and cytosine in complementary DNA sequences  
SO J. Chem. Soc., Chem. Commun. (1993), (9), 800-1  
CODEN: JCCCAT; ISSN: 0022-4936

=> d his

(FILE 'USPAT' ENTERED AT 14:55:23 ON 21 JAN 96)

L1	54138 S SORT###
L2	17725 S #DNA OR POLYNUCLEOTIDE# OR #RNA OR NUCLEIC
L3	1006 S L1 AND L2
L4	323 S L1(P)L2
L5	61 S L1(3A)L2
L6	4224 S OLIGONUCLEOTIDE#
L7	150 S L6 (P) TAG####
L8	28 S L6 (3A) TAG####
L9	93 S (MULTIPLEX OR PARALLEL) (3A) SEQUENCING
L10	31 S L9 AND L2
L11	0 S L8 AND 5451505/PN
L12	29 S L6 (4A)TAG#### NOT L5
L13	4 S HYBRIDIZATION (3A) TAG#
L14	245 S AFFINITY (P) (OLIGONUCLEOTIDE#)
L15	40 S AFFINITY (3A) (OLIGONUCLEOTIDE#)

=> d 3,18,25 cit ab

3. 5,470,710, Nov. 28, 1995, Automated hybridization/imaging device for fluorescent multiplex DNA sequencing; Robert B. Weiss, et al., 435/6, 7.1, 7.5, 7.9 [IMAGE AVAILABLE]

US PAT NO: 5,470,710 [IMAGE AVAILABLE]

L8: 3 of 28

ABSTRACT:

A method is disclosed for automated multiplex sequencing of DNA with an integrated automated imaging hybridization chamber system. This system comprises an hybridization chamber device for mounting a membrane containing size-fractionated multiplex sequencing reaction products, apparatus for fluid delivery to the chamber device, imaging apparatus for light delivery to the membrane and image recording of fluorescence emanating from the membrane while in the chamber device, and programmable controller apparatus for controlling operation of the system. The multiplex reaction products are hybridized with a probe, then an enzyme (such as alkaline phosphatase) is bound to a binding moiety on the probe, and a fluorogenic substrate (such as a benzothiazole derivative) is introduced into the chamber device by the fluid delivery apparatus. The enzyme converts the fluorogenic substrate into a fluorescent product which, when illuminated in the chamber device with a beam of light from the imaging apparatus, excites fluorescence of the fluorescent product to produce a pattern of hybridization. The pattern of hybridization is imaged by a CCD camera component of the imaging apparatus to obtain a series of digital signals. These signals are converted by the controller apparatus into a string of nucleotides corresponding to the nucleotide sequence an automated sequence reader. The method and apparatus are also applicable to other membrane-based applications such as colony and plaque hybridization and Southern, Northern, and Western blots.

18. 5,149,625, Sep. 22, 1992, Multiplex analysis of DNA; George M. Church, et al., 435/6, 172.3, 320.1, 810; 436/808; 935/23, 24, 78 [IMAGE AVAILABLE]

US PAT NO: 5,149,625 [IMAGE AVAILABLE]

L8: 18 of 28

ABSTRACT:

This invention features vectors and a method for sequencing DNA. The method includes the steps of:

- a) ligating the DNA into a vector comprising a tag sequence, the tag sequence includes at least 15 bases, wherein the tag sequence will not hybridize to the DNA under stringent hybridization conditions and is unique in the vector, to form a hybrid vector,
- b) treating the hybrid vector in a plurality of vessels to produce fragments comprising the tag sequence, wherein the fragments differ in

length and terminate at a fixed known base or bases, wherein the fixed known base or bases differs in each vessel,  
c) separating the fragments from each vessel according to their size,  
d) hybridizing the fragments with an oligonucleotide able to hybridize specifically with the tag sequence, and  
e) detecting the pattern of hybridization of the tag sequence, wherein the pattern reflects the nucleotide sequence of the DNA.

25. 4,942,124, Jul. 17, 1990, Multiplex sequencing; George M. Church, 435/6, 172.3, 803; 436/501; 935/23, 24, 29, 77, 78 [IMAGE AVAILABLE]

US PAT NO: 4,942,124 [IMAGE AVAILABLE]

L8: 25 of 28

ABSTRACT:

This invention features vectors and a method for sequencing DNA. The method includes the steps of:

- (a) ligating the DNA into a vector comprising a tag sequence, the tag sequence includes at least 15 bases, wherein the tag sequence will not hybridize to the DNA under stringent hybridization conditions and is unique in the vector, to form a hybrid vector,
- (b) treating the hybrid vector in a plurality of vessels to produce fragments comprising the tag sequence, wherein the fragments differ in length and terminate at a fixed known base or bases, wherein the fixed known base or bases differs in each vessel,
- (c) separating the fragments from each vessel according to their size,
- (d) hybridizing the fragments with an oligonucleotide able to hybridize specifically with the tag sequence, and
- (e) detecting the pattern of hybridization of the tag sequence, wherein the pattern reflects the nucleotide sequence of the DNA.